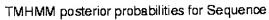
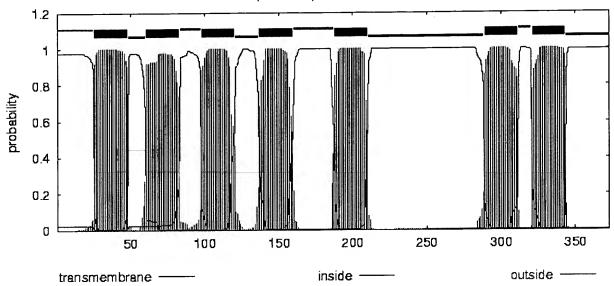
## **APPENDIX 2**





## A. TMHMM result HELP with output formats

***************************************				
# Sequence	Length: 373			
# Sequence	Number of predicte	ed TMHs:	7	
# Sequence	Exp number of AAs	in TMHs:	156.6939	6
# Sequence	Exp number, first	60 AAs:	23.36212	
# Sequence	Total prob of N-in	n:	0.02414	
	POSSIBLE N-term s:		ence	
Sequence	TMHMM2.0	outside	1	25
Sequence	TMHMM2.0	TMhelix	26	48
Sequence	TMHMM2.0	inside	49	60
Sequence	TMHMM2.0	TMhelix	61	83
Sequence	TMHMM2.0	outside	84	97
Sequence	TMHMM2.0	$\mathtt{TMhelix}$	98	120
Sequence	TMHMM2.0	inside	121	136
Sequence	TMHMM2.0	$\mathtt{TMhelix}$	137	159
Sequence	TMHMM2.0	outside	160	187
Sequence	TMHMM2.0	TMhelix	188	210
Sequence	TMHMM2.0	inside	211	288
Sequence	TMHMM2.0	TMhelix	289	311
Sequence	TMHMM2.0	outside	312	320
Sequence	TMHMM2.0	TMhelix	321	343
Sequence	TMHMM2.0	inside	344	373
_				

# plot in postscript, script for making the plot in gnuplot, data for plot

## Conserved Tryptophan and Proline in TM6

**GPCR** 

hARE-2

ghrelin receptor

CXCR3 chemokine receptor

5-hydroxytryptamine (serotonin) receptor 2A

5-hydroxytryptamine (serotonin) receptor 2B

5-hydroxytryptamine (serotonin) receptor 2C

dopamine receptor D3

dopamine receptor D1

histamine receptor H3

galanin receptor 1

neuropeptide Y receptor Y1

neurotensin receptor 1

melanocortin 4 receptor

adenosine A1 receptor

cannabinoid receptor 1

TM6 as predicted by TMHMM

YAITLLFLLLWSPYIVACYWRVF

MLAVVVFAFILCWL**P**FHVGRYLF

LVVVVVVAFALCWTPYHLVV

LGIVFFLFVVM**W**C**P**FFITNIMAV

GIVFFLFLLMWCPFFITNITLVL

VLGIVFFVFLIMWCPFFITNILS

VAIVLGAFIVCWLPFFLTHVLNT

TLSVIMGVFVCCWLPFFILNCIL

**AVIVSIFGLCWAPYTLLMIIRAA** 

TVLVVVVVFGISWLPHHIIHLWA

**IMLLSIVVAFAVCWLPLTIFNTV** 

VLRAVVIAFVVC**W**L**P**YHVRRLMF

**ITLTILIGVFVVCWAPFFLHLIF** 

LALILFLFALSWLPLHILNCITL

LVLILVVLIICWGPLLAIMVYDV